RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/588,565
Source: IFWP
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IFWP

RAW SEQUENCE LISTING DATE: 08/14/2006
PATENT APPLICATION: **US/10/588,565** TIME: 13:56:47

Input Set : **A:\CIBT-PWO-175 Sub Sequence Listing.txt**
Output Set: **N:\CRF4\08142006\J588565.raw**

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      3 <110> APPLICANT: Curis, Inc.
      4       Benvenisty, Nissim
      5       Eiges, Rachel
      7 <120> TITLE OF INVENTION: GENE PROFILING OF HUMAN EMBRYONIC STEM CELLS
      9 <130> FILE REFERENCE: CIBT-PWO-175
C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/588,565
C--> 12 <141> CURRENT FILING DATE: 2006-08-04
     14 <150> PRIOR APPLICATION NUMBER: US 60/542,451
     15 <151> PRIOR FILING DATE: 2004-02-06
     17 <160> NUMBER OF SEQ ID NOS: 30
     19 <170> SOFTWARE: PatentIn version 3.2
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     23 <212> TYPE: DNA
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     57 tgcagaaaga actcgagcaa tttgccaagc tcctgaagca gaagaggatc accctgggat    960
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83 gaacacaaag ggtgggggca ggggagtttg gggcaactgg ttggagggaa ggtgaagttc   1740
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102             20                  25                  30
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106         35                  40                  45
109 Lys Glu Leu Glu Gln Phe Ala Lys Leu Leu Lys Gln Lys Arg Ile Thr
110     50                  55                  60
113 Leu Gly Tyr Thr Gln Ala Asp Val Gly Leu Thr Leu Gly Val Leu Phe
114 65                  70                  75                  80
117 Gly Lys Val Phe Ser Gln Thr Thr Ile Cys Arg Phe Glu Ala Leu Gln
118                 85                  90                  95
121 Leu Ser Phe Lys Asn Met Cys Lys Leu Arg Pro Leu Leu Gln Lys Trp
122             100                 105                 110
125 Val Glu Glu Ala Asp Asn Asn Glu Asn Leu Gln Glu Ile Cys Lys Ala
126         115                 120                 125
129 Glu Thr Leu Val Gln Ala Arg Lys Arg Lys Arg Thr Ser Ile Glu Asn
130     130                 135                 140
133 Arg Val Arg Gly Asn Leu Glu Asn Leu Phe Leu Gln Cys Pro Lys Pro
134 145                 150                 155                 160
137 Thr Leu Gln Gln Ile Ser His Ile Ala Gln Gln Leu Gly Leu Glu Lys
138                 165                 170                 175
141 Asp Val Val Arg Val Trp Phe Cys Asn Arg Arg Gln Lys Gly Lys Arg
142             180                 185                 190
145 Ser Ser Ser Asp Tyr Ala Gln Arg Glu Asp Phe Glu Ala Ala Gly Ser
146         195                 200                 205
149 Pro Phe Ser Gly Gly Pro Val Ser Phe Pro Leu Ala Pro Gly Pro His
150     210                 215                 220
153 Phe Gly Ala Pro Gly Tyr Gly Ser Pro His Phe Thr Ala Leu Tyr Ser
154 225                 230                 235                 240
157 Ser Val Pro Phe Pro Glu Gly Glu Ala Phe Pro Pro Val Ser Val Thr
158                 245                 250                 255
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166 <211> LENGTH: 2386
167 <212> TYPE: DNA
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177 aacagcctcg ttgctcacac aaagcctgtt tggtggtctc ttcacacgga cgcgcatgaa   240
179 atttggtgcc gtgactcgga tcgggggacc tcccttggga gatcaatccc ctgtcctcct   300
181 gctctttgct ccgtgagaaa gatccaccta cgacctcagg tcctcagacc aaccagccca   360
183 agaaacatct caccaatttc aaatccggta agcggcctct ttttactctg ttctccaacc   420
185 tccctcacta tccctcaacc tctttctcct ttcaatcttg gcgccacact tcaatctctc   480
187 ccttctctta atttcaattc ctttcattct ctggtagaga caaaagagac atgttttatc   540
189 cgtgaaccca aaactccggc gccggtcacg gactgggaag gcagtcttcc cttggtgttt   600
191 aatcattgca gggacgcctc tctgatttca cgtttcagac cacgcaggga tgcctgcctt   660
193 ggtccttcac ccttagcggc aagtcccgct ttcctggggc aggggcaagt acccctcaac   720
195 cccttctcct tcacccttag cggcaagtcc cgcttttctg gggcaggggc aagtacccct   780
197 caacccccttc tccttcaccc ttagcagcaa gtcccgcttt cctaggggggc aagaacccccc   840
199 caatcgctta ttttcacgcc ccaacagaaa cccccacccc ttctccgtgt ctctactctt   900
201 ttctctgggc ttgcctcctt cactatgggc aagcttccac cttccattcc tttcttctcc   960
203 cttagcatgt attcttaaga acttaaaatc tcttcaattc tcacctgacc taaaatctaa  1020
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207 atagccagaa aatggcactt tcaatttttc caccctacaa gatctaaata attcttggcg  1140
209 taaaatgggc aaatggtgtg aggtgcctga cgtccaggca ttcttttaca catcagtccc  1200
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215 catctgacct ctcccttcct ccccaggctg ctccttgcca ggccgagcta ggtcccaatt  1380
217 cttcctcagc ctcacacaag aacttccaaa cgcctgaact gtagcagcca gacgtttctc  1440
219 cagaacctcc tcccccagga acttgctaca catgccggaa atctggccac tgggccaagg  1500
221 aacgcccgca gcccgggatt cctcctaagc cgcgtcccat ctgtgtggga ccccactgaa  1560
223 aatcggactg ttcaactcac ctggcagcca ctcccagagc tcctggaact ctggcccaag  1620
225 gttctctgac tgactccttc ttggcttact ggctgaagac tgacgctgcc tgatcgcctc  1680
227 agaagccccg cagaccatca tggacgccga gctttagccc gcctgcaccc aggtgaaata  1740
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241 ttcaggtcac agaagcttca aggggaaaaa aacagaatac tctagggcca ttgttcacaa  2160
243 actcatctga aaacatcctg gaaaaatttt cccaaacaca tggaaagaaa gagaggaaaa  2220
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247 aacagtactt tcttctctgg ctgagtccct ggtattctct gctgcaatct gtagctgtag  2340
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254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapiens
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263 Phe Ser Asp Ser Ala Arg Leu His Pro Gly Glu Ile Asn Ser Leu Val
264             20                  25                  30
267 Ala His Thr Lys Pro Val Trp Trp Ser Leu His Thr Asp Ala His Glu
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272     50                  55                  60
275 Pro Cys Pro Pro Ala Leu Cys Ser Val Arg Lys Ile His Leu Arg Pro
276 65                  70                  75                  80
279 Gln Val Leu Arg Pro Thr Ser Pro Arg Asn Ile Ser Pro Ile Ser Asn
280                 85                  90                  95
283 Pro Val Ser Gly Leu Phe Leu Leu Cys Ser Pro Thr Ser Leu Thr Ile
284             100                 105                 110
287 Pro Gln Pro Leu Ser Pro Phe Asn Leu Gly Ala Thr Leu Gln Ser Leu
288         115                 120                 125
291 Pro Ser Leu Asn Phe Asn Ser Phe His Ser Leu Val Glu Thr Lys Glu
292     130                 135                 140
295 Thr Cys Phe Ile Arg Glu Pro Lys Thr Pro Ala Pro Val Thr Asp Trp
296 145                 150                 155                 160
299 Glu Gly Ser Leu Pro Leu Val Phe Asn His Cys Arg Asp Ala Ser Leu
300                 165                 170                 175
303 Ile Ser Arg Phe Arg Pro Arg Arg Asp Ala Cys Leu Gly Pro Ser Pro
304             180                 185                 190
307 Leu Ala Ala Ser Pro Ala Phe Leu Gly Gln Gly Gln Val Pro Leu Asn
308         195                 200                 205
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333 accaatttca aatctggacc ccactgaaaa tcggactgtt caactcatct ggcagccact    300
335 cccagagccc ctggaactct ggcccaagcc tctctgactg actccttccc agatcttctc    360
337 ggcttagcag ctgaagactg acactgccca atcgccttgg aagcccccta gaccatcacg    420
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353 actcaaggat tggactcatt cttttgttcc atgaatgcca attctgcaga agccactgtg    900
355 gtagaaattc aaatgtaatg aaaaacaaac attcactcat ttattatcac tatttgcctg    960
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360 <210> SEQ ID NO: 6
361 <211> LENGTH: 111
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371 Asn Ser Leu Val Ala His Thr Lys Pro Val Trp Trp Ser Leu His Thr
372 20 25 30
375 Asn Ala His Glu Ile Trp Cys His Asp Ser Asp Arg Gly Thr Ser Leu
376 35 40 45
379 Gly Arg Ser Ile Pro Ser Pro Pro Ala Leu Cys Ser Val Arg Lys Ile
380 50 55 60
383 Tyr Leu Gly Pro Gln Val Leu Arg Leu Thr Ser Pro Arg Asn Ile Ser
384 65 70 75 80
387 Pro Ile Ser Asn Leu Asp Pro Thr Glu Asn Arg Thr Val Gln Leu Ile
388 85 90 95
391 Trp Gln Pro Leu Pro Glu Pro Leu Glu Leu Trp Pro Lys Pro Leu
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396 <211> LENGTH: 3459
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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date